

PCT/10
Rec'd PCT/PTO 21 SEP 2004

**CRF Errors Edited by the STIC Systems
Branch**

10/507082

Serial Number: 10/507,082

CRF Edit Date: 9/21/04
Edited by: 12

Realigned nucleic acid/amino acid numbers/text in cases where the sequence
text "wrapped" to the next line

ENTERED

Corrected the SEQ ID NO. Sequence numbers edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID
NO's edited:

Deleted: invalid beginning/end-of-file text ; page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT10

RAW SEQUENCE LISTING

DATE: 09/21/2004

PATENT APPLICATION: US/10/507,082

TIME: 22:03:13

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09212004\J507082.raw

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5 <110> APPLICANT: SmithKline Beecham Corporation
6      CuraGen Corporation
10 <120> TITLE OF INVENTION: Methods of Using Farnesoid X Receptor (FXR) Agonists
14 <130> FILE REFERENCE: PU4692WO
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/507,082
C--> 16 <141> CURRENT FILING DATE: 2004-09-09
16 <150> PRIOR APPLICATION NUMBER: 60/366,463
17 <151> PRIOR FILING DATE: 2002-03-21
21 <160> NUMBER OF SEQ ID NOS: 2
25 <170> SOFTWARE: PatentIn version 3.1
29 <210> SEQ ID NO: 1
31 <211> LENGTH: 2157
33 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
41 <221> NAME/KEY: CDS
43 <222> LOCATION: (464)..(1114)
45 <223> OTHER INFORMATION:
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50 gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc      60
52 cgctaagcga ggcctcctcc tccgcagat ccgaacggcc tgggcgggggt caccctggct      120
54 gggacaagaa gccgcgcct gctgcccgg gcccggggag ggggctgggg ctggggccgg      180
56 aggcgggggtg tgagtgggtg tgtgcgggg gcgaggctt gatgcaatcc cgataagaaa      240
58 tgctcgggtg tcttgggcac ctaccctgg ggcccgtaag gcgctactat ataaggctgc      300
60 cggcccggag ccgccgcgcc gtcagagcag gagcgctgcg tccaggatct agggccacga      360
62 ccatcccaac ccggcactca cagccccgca gcgcattccg gtcgccgccc agcctccgcg      420
64 acccccatcg ccggagctgc gccgagagcc ccaggagggt gcc atg cgg agc ggg      475
65                                     Met Arg Ser Gly
66                                     1
68 tgt gtg gtg gtc cac gta tgg atc ctg gcc ggc ctc tgg ctg gcc gtg      523
69 Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu Trp Leu Ala Val
70 5          10          15          20
72 gcc ggg cgc ccc ctc gcc ttc tcg gac gcg ggg ccc cac gtg cac tac      571
73 Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro His Val His Tyr
74          25          30          35
76 ggc tgg ggc gac ccc atc cgc ctg cgg cac ctg tac acc tcc ggc ccc      619
77 Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr Thr Ser Gly Pro
78          40          45          50
80 cac ggg ctc tcc agc tgc ttc ctg cgc atc cgt gcc gac ggc gtc gtg      667
81 His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala Asp Gly Val Val
82          55          60          65
84 gac tgc gcg cgg ggc cag agc gcg cac agt ttg ctg gag atc aag gca      715
85 Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu Glu Ile Lys Ala

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86      70      75      80
88 gtc gct ctg cgg acc gtg gcc atc aag ggc gtg cac agc gtg cgg tac      763
89 Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His Ser Val Arg Tyr
90 85      90      95      100
92 ctc tgc atg ggc gcc gac ggc aag atg cag ggg ctg ctt cag tac tcg      811
93 Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser
94      105      110      115
96 gag gaa gac tgt gct ttc gag gag gag atc cgc cca gat ggc tac aat      859
97 Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn
98      120      125      130
100 gtg tac cga tcc gag aag cac cgc ctc ccg gtc tcc ctg agc agt gcc      907
101 Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala
102      135      140      145
104 aaa cag cgg cag ctg tac aag aac aga ggc ttt ctt cca ctc tct cat      955
105 Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His
106      150      155      160
108 ttc ctg ccc atg ctg ccc atg gtc cca gag gag cct gag gac ctc agg      1003
109 Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg
110 165      170      175      180
112 ggc cac ttg gaa tct gac atg ttc tct tcg ccc ctg gag acc gac agc      1051
113 Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp Ser
114      185      190      195
116 atg gac cca ttt ggg ctt gtc acc gga ctg gag gcc gtg agg agt ccc      1099
117 Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg Ser Pro
118      200      205      210
120 agc ttt gag aag taa ctgagaccat gcccgggcct cttcactgct gccaggggct      1154
121 Ser Phe Glu Lys
122      215
124 gtggtacctg cagcgtgggg gacgtgcttc tacaagaaca gtcctgagtc cacgttctgt      1214
126 ttagcttttag gaagaaacat ctagaagttg tacatatcca gagttttcca ttggcagtgc      1274
128 cagttttctag ccaatagact tgtctgatca taacattgta agcctgtagc ttgccagct      1334
130 gctgcctggg cccccattct gctccctcga ggttgctgga caagctgctg cactgtctca      1394
132 gttctgcttg aatacctcca tcgatgggga actcacttcc tttggaaaaa ttcttatgtc      1454
134 aagctgaaat tctctaattt tttctcatca cttccccagg agcagccaga agacaggcag      1514
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146 accagccctc tgcccacctc acatgcctcc ccattggattg gggcctccca ggccccccac      1874
148 cttatgtcaa cctgcacttc ttgttcaaaa atcaggaaaa gaaaagattt gaagacccca      1934
150 agtcttgtca ataacttgct gtgtggaagc agcgggggaa gacctagaac cttttcccca      1994
152 gcacttggtt ttccaacatg atatttatga gtaatttatt ttgatatgta catctcttat      2054
154 tttcttacat tatttatgcc cccaaattat atttatgtat gtaagtgagg tttgttttgt      2114
156 atattaaaat ggagtttgtt tgtaaaaaaa aaaaaaaaaa aaa      2157
159 <210> SEQ ID NO: 2
161 <211> LENGTH: 216
163 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens

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169 <400> SEQUENCE: 2

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171 Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
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175 Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
176          20          25          30
179 His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
180          35          40          45
183 Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
184          50          55          60
187 Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
188 65          70          75          80
191 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
192          85          90          95
195 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
196          100          105          110
199 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
200          115          120          125
203 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
204          130          135          140
207 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
208 145          150          155          160
211 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
212          165          170          175
215 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
216          180          185          190
219 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
220          195          200          205
223 Val Arg Ser Pro Ser Phe Glu Lys
224          210          215

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:49 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:45